

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Loetscher, Marcel  
Moser, Bernhard
- (ii) TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,  
NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
  - (B) STREET: Two Militia Drive
  - (C) CITY: Lexington
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02173
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brook Esq., David E.
  - (B) REGISTRATION NUMBER: 22,592
  - (C) REFERENCE/DOCKET NUMBER: TK196-01
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 861-6240
  - (B) TELEFAX: (617) 861-9540

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1670 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 69..1172

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAACCACAA GCACCAAAGC AGAGGGGCAG GCAGCACACC ACCCAGCAGC CAGAGCACCA	60
GGCCAGCC ATG GTC CTT GAG GTG AGT GAC CAC CAA GTG CTA AAT GAC GCC	110
Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala	
1 5 10	

GAG Glu 15	GTT Val	GCC Ala	GCC Ala	CTC Leu	CTG Leu 20	GAG Glu	AAC Asn	TTC Phe	AGC Ser	TCT Ser 25	TCC Ser	TAT Tyr	GAC Asp	TAT Tyr	GGA Gly 30	158
GAA Glu	AAC Asn	GAG Glu	AGT Ser	GAC Asp 35	TCG Ser	TGC Cys	TGT Cys	ACC Thr	TCC Ser 40	CCG Pro	CCC Pro	TGC Cys	CCA Pro	CAG Gln 45	GAC Asp	206
TTC Phe	AGC Ser	CTG Leu	AAC Asn 50	TTC Phe	GAC Asp	CGG Arg	GCC Ala	TTC Phe 55	CTG Leu	CCA Pro	GCC Ala	CTC Leu	TAC Tyr 60	AGC Ser	CTC Leu	254
CTC Leu	TTT Phe	CTG Leu 65	CTG Leu	GGG Gly	CTG Leu	CTG Leu	GGC Gly 70	AAC Asn	GGC Gly	GCG Ala	GTG Val	GCA Ala 75	GCC Ala	GTG Val	CTG Leu	302
CTG Leu 80	AGC Ser	CGG Arg	CGG Arg	ACA Thr	GCC Ala	CTG Leu 85	AGC Ser	AGC Ser	ACC Thr	GAC Asp 90	ACC Thr	TTC Phe	CTG Leu	CTC Leu	CAC His	350
CTA Leu 95	GCT Ala	GTA Val	GCA Ala	GAC Asp	ACG Thr 100	CTG Leu	CTG Leu	GTG Val	CTG Leu	ACA Thr 105	CTG Leu	CCG Pro	CTC Leu	TGG Trp	GCA Ala 110	398
GTG Val	GAC Asp	GCT Ala	GCC Ala	GTC Val 115	CAG Gln	TGG Trp	GTC Val	TTT Phe	GGC Gly 120	TCT Ser	GGC Gly	CTC Leu	TGC Cys	AAA Lys 125	GTG Val	446
GCA Ala	GGT Gly	GCC Ala	CTC Leu 130	TTC Phe	AAC Asn	ATC Ile	AAC Asn	TTC Phe 135	TAC Tyr	GCA Ala	GGA Gly	GCC Ala	CTC Leu 140	CTG Leu	CTG Leu	494
GCC Ala	TGC Cys	ATC Ile 145	AGC Ser	TTT Phe	GAC Asp	CGC Arg	TAC Tyr 150	CTG Leu	AAC Asn	ATA Ile	GTT Val	CAT His 155	GCC Ala	ACC Thr	CAG Gln	542
CTC Leu 160	TAC Tyr	CGC Arg	CGG Arg	GGG Gly	CCC Pro	CCG Pro 165	GCC Ala	CGC Arg	GTG Val	ACC Thr	CTC Leu 170	ACC Thr	TGC Cys	CTG Leu	GCT Ala	590
GTC Val 175	TGG Trp	GGG Gly	CTC Leu	TGC Cys 180	CTG Leu	CTT Leu	TTC Phe	GCC Ala	CTC Leu	CCA Pro 185	GAC Asp	TTC Phe	ATC Ile	TTC Phe	CTG Leu 190	638
TCG Ser	GCC Ala	CAC His	CAC His	GAC Asp 195	GAG Glu	CGC Arg	CTC Leu	AAC Asn 200	GCC Ala	ACC Thr	CAC His	TGC Cys	CAA Gln	TAC Tyr 205	AAC Asn	686
TTC Phe	CCA Pro	CAG Gln 210	GTG Val	GGC Gly	CGC Arg	ACG Thr	GCT Ala	CTG Leu 215	CGG Arg	GTG Val	CTG Leu	CAG Gln 220	CTG Leu	GTG Val	GCT Ala	734
GGC Gly	TTT Phe	CTG Leu 225	CTG Leu	CCC Pro	CTG Leu	CTG Leu	GTC Val 230	ATG Met	GCC Ala	TAC Tyr	TGC Cys	TAT Tyr 235	GCC Ala	CAC His	ATC Ile	782
CTG Leu 240	GCC Ala	GTG Val	CTG Leu	CTG Leu	GTT Val	TCC Ser 245	AGG Arg	GGC Gly	CAG Gln	CGG Arg	CGC Arg	CTG Leu	CGG Arg	GCC Ala	ATG Met	830

CGG CTG GTG GTG GTG GTC GTG GTG GCC TTT GCC CTC TGC TGG ACC CCC 878  
 Arg Leu Val Val Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro  
 255 260 265 270

TAT CAC CTG GTG GTG CTG GTG GAC ATC CTC ATG GAC CTG GGC GCT TTG 926  
 Tyr His Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu  
 275 280 285

GCC CGC AAC TGT GGC CGA GAA AGC AGG GTA GAC GTG GCC AAG TCG GTC 974  
 Ala Arg Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val  
 290 295 300

ACC TCA GGC CTG GGC TAC ATG CAC TGC TGC CTC AAC CCG CTG CTC TAT 1022  
 Thr Ser Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr  
 305 310 315

GCC TTT GTA GGG GTC AAG TTC CGG GAG CGG ATG TGG ATG CTG CTC TTG 1070  
 Ala Phe Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu  
 320 325 330

CGC CTG GGC TGC CCC AAC CAG AGA GGG CTC CAG AGG CAG CCA TCG TCT 1118  
 Arg Leu Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser  
 335 340 345 350

TCC CGC CGG GAT TCA TCC TGG TCT GAG ACC TCA GAG GCC TCC TAC TCG 1166  
 Ser Arg Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser  
 355 360 365

GGC TTG TGAGGCCGGA ATCCGGGCTC CCCTTTCGCC CACAGTCTGA CTTCCCCGCA 1222  
 Gly Leu

TTCCAGGCTC CTCCCTCCCT CTGCCGGCTC TGGCTCTCCC CAATATCCTC GCTCCCGGGA 1282

CTCACTGGCA GCCCCAGCAC CACCAGGTCT CCCGGGAAGC CACCCTCCCA GCTCTGAGGA 1342

CTGCACCATT GCTGCTCCTT AGCTGCCAAG CCCCATCCTG CCGCCCGAGG TGGCTGCCTG 1402

GAGCCCCACT GCCCTTCTCA TTTGGAAACT AAAACTTCAT CTTCCCCAAG TGCGGGGAGT 1462

ACAAGGCATG GCGTAGAGGG TGCTGCCCCA TGAAGCCACA GCCCAGGCCT CCAGCTCAGC 1522

AGTGACTGTG GCCATGGTCC CCAAGACCTC TATATTTGCT CTTTTATTTT TATGTCTAAA 1582

ATCCTGCTTA AACTTTTCA ATAAACAAGA TCGTCAGGAC CTTTTTTTTT TTTTTTTTTT 1642

TTTTTTTTTT TTTTTTTTTT TTTTTTTT 1670

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

0062230 "EST" 0950

Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val  
 1 5 10 15  
 Ala Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn  
 20 25 30  
 Glu Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser  
 35 40 45  
 Leu Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe  
 50 55 60  
 Leu Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser  
 65 70 75 80  
 Arg Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala  
 85 90 95  
 Val Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp  
 100 105 110  
 Ala Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly  
 115 120 125  
 Ala Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys  
 130 135 140  
 Ile Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr  
 145 150 155 160  
 Arg Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp  
 165 170 175  
 Gly Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala  
 180 185 190  
 His His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro  
 195 200 205  
 Gln Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe  
 210 215 220  
 Leu Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala  
 225 230 235 240  
 Val Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu  
 245 250 255  
 Val Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His  
 260 265 270  
 Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg  
 275 280 285  
 Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser  
 290 295 300  
 Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe  
 305 310 315 320  
 Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu  
 325 330 335

006630"05F20660

Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu  
355 360 365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(A) NAME/KEY: modified base

- (B) LOCATION: 11  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified base

- (B) LOCATION: 12  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified base

- (B) LOCATION: 23  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified base

- (B) LOCATION: 26  
(D) OTHER INFORMATION: /mod base= i

GGGCTGCAGC NNTKKCMGAC MTNCTNYT

28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(A) NAME/KEY: modified base

- (B) LOCATION: 10  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified base

- (B) LOCATION: 16  
(D) OTHER INFORMATION: /mod base= i

[illegible]

(B) LOCATION: 18

(D) OTHER INFORMATION: /mod base= 1

[illegible][illegible]